SEQUENCE LISTING

```
<110> Loughney, Kate
<120> Phosphodiesterase 10
<130> 27866/35308
<140> 09/256,000
<141> 1999-02-23
<150> 60/075,508
<151> 1998-02-23
<160> 26
<170> PatentIn Ver. 2.0
<210> 1
<211> 1548
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> (26)..(1423)
cccaaqqcca tctacctgga catcg atg gac gca ttc aga agc act ccg tac
                            Met Asp Ala Phe Arg Ser Thr Pro Tyr
aaa gtg aga cct gtg gcc atc aag caa ctc tcc gag aga gaa gaa tta
Lys Val Arg Pro Val Ala Ile Lys Gln Leu Ser Glu Arg Glu Glu Leu
atc cag agc gtg ctg gcg cag gtt gca gag cag ttc tca aga gca ttc
Ile Gln Ser Val Leu Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe
aaa atc aat gaa ctg aaa gct gaa gtt gca aat cac ttg gct gtc cta
                                                                   196
Lys Ile Asn Glu Leu Lys Ala Glu Val Ala Asn His Leu Ala Val Leu
                                 50
gag aaa cgc gtg gaa ttg gaa gga cta aaa gtg gtg gag att gag aaa
Glu Lys Arg Val Glu Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys
                             65
tgc aag agt gac att aag aag atg agg gag gag ctg gcg gcc aga agc
                                                                   292
Cys Lys Ser Asp Ile Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser
                         80
age agg acc aac tge eec tgt aag tac agt ttt ttg gat aac cac aag
                                                                   340
Ser Arg Thr Asn Cys Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys
                                         100
                     95
aag ttg act cct cga cgc gat gtt ccc act tac ccc aag tac ctg ctc
                                                                   388
Lys Leu Thr Pro Arg Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu
```

110 115 120

| | | gag Glu | | | | | | | | | | | | | | 436 |
|------------|------------|-------------------|------------|-------------------|------------|------------|------------|------------|-------------------|------------|------------|------------|------------|-------------------|------------|------|
| | | gag Glu 140 | | | | | | | | | | | | | | 484 |
| | | gly ggg | | | | | | | | | | | | | | 532 |
| | | ctg Leu | | | | | | | | | | | | | | 580 |
| aac Asn | ttc Phe | cgg Arg | cac His | tgc Cys 190 | ttc Phe | tgc Cys | gtg Val | gcc Ala | cag Gln 195 | atg Met | atg Met | tac Tyr | agc Ser | atg Met 200 | gtc Val | 628 |
| | | tgc Cys | | | | | | | | | | | | | | 676 |
| | | aca Thr 220 | | | | | | | | | | | | | | 724 |
| | | tac Tyr | | | | | | | | | | | | | | 772 |
| _ | Ile | tca Ser | | _ | - | | | | _ | _ | _ | _ | | | | 820 |
| | | gag Glu | | | | | | | | | | | | | | 868 |
| | | cag Gln | | Arg | Gln | Gly | Met | | Thr | Leu | Ile | Leu | Ăla | Thr | | 916 |
| | | aga Arg 300 | | | | | | | | | | | | | | 964 |
| | | gac Asp | | | | | | | | | | | | | | 1012 |
| | | aaa Lys | | | | | | | | | | | | | | 1060 |

| _ | gag Glu | | | | _ | _ | | | | _ | | | - | _ | - | 1108 |
|------------|---------------------------------|-----------|-----------|----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|--------|------|
| | cgt Arg | | | | | | | | | | | | | | | 1156 |
| | aaa Lys | | | | | | | | | | | | | | | 1204 |
| | atc Ile 395 | | | | | | | | | | | | | | | 1252 |
| | atc Ile | | | | | | | | | | | | | | | 1300 |
| _ | aag Lys | | | - | _ | - | _ | | | | _ | _ | _ | | | 1348 |
| | ttg Leu | | | | | | | | | | | | | | | 1396 |
| | aaa Lys | | | | | | | | tgag | ggaaa | agc g | 3333 | ggcgt | cg | | 1443 |
| gct | gcagt | itc t | ggad | cggg | ct go | gccga | agcto | g cg | ggga | atcc | ttgt | gcag | ggg 8 | aagag | gctgcc | 1503 |
| ctg | ggca | cct q | ggca | ccaca | aa ga | accat | gtt | tct | aaga | aacc | att | t | | | | 1548 |
| <21 <21 | 0> 2 l> 46 2> PI 3> Ho | RT | sapie | ens | | | | | | | | | | | | |
| | 0> 2 Asp | Ala | Phe | Arg 5 | Ser | Thr | Pro | Tyr | Lys 10 | Val | Arg | Pro | Val | Ala 15 | Ile | |
| Lys | Gln | Leu | Ser 20 | Glu | Arg | Glu | Glu | Leu 25 | Ile | Gln | Ser | Val | Leu 30 | Ala | Gln | |
| Val | Ala | Glu 35 | Gln | Phe | Ser | Arg | Ala 40 | Phe | Lys | Ile | Asn | Glu 45 | Leu | Lys | Ala | |
| Glu | Val 50 | Ala | Asn | His | Leu | Ala 55 | Val | Leu | Glu | Lys | Arg 60 | Val | Glu | Leu | Glu | |
| Gly 65 | Leu | Lys | Val | Val | Glu 70 | Ile | Glu | Lys | Cys | Lys 75 | Ser | Asp | Ile | Lys | Lys | |

Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn Cys Pro Cys
85 90 95

Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro Arg Arg Asp 100 105 110

Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr Ile Glu Ala 115 120 125

Leu Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro Asn Glu Met 130 135 140

Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu Val Arg Asp 145 150 155 160

Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe Cys Val His
165 170 175

Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys Phe Cys 180 185 190

Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu Gln Glu 195 200 205

Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala Ile Cys 210 215 220

His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile Asn Ala 225 230 235 240

Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu Glu Asn 245 250 255

His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu Cys Asn 260 265 270

Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg Gln Gly 275 280 285

Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala Glu Ile 290 295 300

Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser Asn Glu 305 310 315 320

Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile 325 330 335

Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val Asp Cys 340 345 350

Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys Ser Glu Gly 355 360 365

Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys Ala Thr 370 375 380

Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe Glu Thr

385 390 395 400

Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln Pro Leu 405 410 415

Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala 420 425 430

Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala Thr 435 440 445

Glu Lys Ser Arg Gly Arg Ser Arg Asp Val Lys Asn Ser Glu Gly Asp 450 460

Cys Ala 465

<210> 3

<211> 225

<212> DNA

<213> Homo sapiens

<220>

<223> Nucleotides at positions 130, 186, and 205 are either A, T, G, or C.

<400> 3
agcgaccgtg agaagtcaga aggccttcct gtggaaccgt tcatggaccg agacaaagtg 60
accaaggcca cagcccagat tgggttcatc aagtttgccc tgatcccaat gtttgaaaca 120
gtgaccaagn tcttccccat ggttgaggag atcatgctgc agccactttg ggaatcccga 180
gatcgntacg aggagctgaa gcggntagat gacgccatga aagag
225

<210> 4

<211> 158

<212> DNA

<213> Homo sapiens

<220>

<223> Nucleotides at positions 12, 36, 61, and 109 are either A, T, G, or C.

<400> 4

gtaccagatc antgcccgca cagagctggc ggtccgntac aatgacatct caccgttgga 60 gnaaccacca ctgcgccgtg gccttccaga tcctcgccga gcctgagtgn aacatcttct 120 ccaacatccc acctgatggg ttcaagcaga tccgacag 158

<210> 5

<211> 98

<212> DNA

<213> Homo sapiens

```
<220>
<223> Nucleotides at positions 14, 22, and 50 are either
      A, T, C, or G.
<400> 5
gagaacacca ctgngccgtg gncttccaga tcctcgccga gcctgagtgn aacatcttct 60
                                                                  98
ccaacatccc acctgatggg ttcaagcaga tccgacag
<210> 6
<211> 418
<212> DNA
<213> Homo sapiens
<220>
<223> Nucleotides at positions 1, 267, 352, 400, and 411
     are either A, T, G, or C.
<400> 6
ngqttaactg gcgcatcttg tctttctctg agaacagcga tctggttatg gggcatttct 60
gtctctaatg tcactgtctg ctgcattccc tgcagagcga ccgtgagaag tcagaaggcc 120
ttcccgtqqc cccgttcatg gaccgagaca aagtgaccaa ggccacagcc caggattggg 180
tttcatcaag tttgtcctga tcccaatgtt tgaaacagtg accaagctct tccccatggg 240
ttgagggaga ttcatgctgg cagccanttt ggggaatccc gaggattcgc tacgagggag 300
cttgaagcgg gattaggatg gacggccatg gaaaggagtt ttacaggaag gnaggatttg 360
acagttttga agttttgggg gggccaccga ggaagttccn ggaggaggag naggcaga
<210> 7
<211> 428
<212> DNA
<213> Homo sapiens
<220>
<223> Nucleotides at positions 1, 82. 92, 130, 347, 390,
      and 396 are either A, T, G, or C.
<400> 7
nagaaaaaag tgaacaaaat ggttcttaga aaacatggtc ttgtggtgcc aggtgcccag 60
ggagetette cetgeacaag gnteeegege anteggeeag eeegteeaga actgeageea 120
egececegn ttteeteagg cacagtetee tteaetgttt tteaeatete tgettetete 180
tetggaette teggtggeee eagaegteaa getgteagte ttettetgta aetettteat 240
gggcgtcatc tatccgcttc agctcctcgt aggcgatctc ggggattccc aaagtgggct 300
gcagcatgat cttcctcaac catgggggg aggagcttgg ggcactngtt ttcaaaaatt 360
```

gggggatcag gggacaaact ttgattggan cccatnttgg ggcttttggg cctttggggc 420

aatttttg 428

tttttttt tttttttt tttttttgt atcagtgaac aaaatggttc ttagaaaaca tggtcttgtg 60 gtnccaggtg cccagggage tettecetge acaaggance cgcgcantcg gccagcccgt 120 ccagaactgc agccacgccc cccgttttcc tcaggcacag tctccttcac tgtttttcac 180 atctctgntt ctctctctgg ganttntcgg tgggccccag aacgtcaage tgtcagtntt 240 cttctgtaac tntttcatgg gcgtcatcta tccgtttcag cttcctcgta ggcgatnttg 300 gggattccca aagtgggctg gcagcatgga tcttcctcaa accatggggg gaaggagttt 360 gggtcaattn ttttcaaaac attgggggnt cagggacaaa attttgatgg aaacccaatt 420 tgggggntgt gggccttg

<210> 9 <211> 262 <212> DNA <213> Mus musculus

<400> 9
gagaattttg actacagcaa cgaggagcac ctgaccctgc tgaagatgat tctcataaaa 60
tgctgtgata tctccaatga agtccgtccc atggaggtgg cagaatcgtg ggtggactgt 120
ttactggaag aatattttat gcagagtgac cgtgagaagt ccgaagcctt cctgtggccc 180
cattcatgga ccgagacaaa gtgaccaaag caacagccca aattgggttc atcaagtttg 240
tcctgatccc aatgtttgaa ac
262

<210> 10 <211> 250 <212> DNA <213> Mus musculus

<400> 10
gagaattttg actacagcaa cgaggagcac ctgaccctgc tgaagatgat tctcataaaa 60
tgctgtgata tctccaatga agtccgtccc atggaggtgg cagaatcgtg ggtggactgt 120

```
ttactggaag aatattttat gcagagtgac cgtgagaagt ccgaagcctt cctgtggccc 180
attcatggac cgagacaaag tgaccaaagc aacagccaaa ttgggttcat caagtttgtc 240
                                                                   250
tgtccaatgt
<210> 11
<211> 459
<212> DNA
<213> Homo sapiens
<220>
<223> Nucleotides at positions 155, 393, and 442 are
      either A, T, G, or C.
<400> 11
attaatcttg gccactgaca tggcaagaca tgcagaaatt atggattctt tcaaagagaa 60
aatqqaqaat tttgactaca gcaacgagga gcacatgacc ctggtgagtg gcttattctg 120
cctgggtggg cagccaggcg gttgggctgg cgaanaggtt catccatcca gctcacactg 180
gaagccaaga agctgaaatt attagtcttc ttggaacaag gtgtctataa atctggtttt 240
caaggtcatg actottacta ggaaagtccg ggcagggcct coctoctgat gggtcctcct 300
tcatggtcag aggcagcatt ctcccattcc tccatctctt ttgggatttt gaaggagata 360
aagtggggtg aaggeegtge attetegete tgntttteea gagaattaaa accagtttte 420
ccttgaaggc acagccccag cntggcattt tgaaagttg
                                                                   459
<210> 12
<211> 599
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> (99)..(443)
tqqccctcga qgccaagaat tcggcacgag tggttaactg gcgcatcttg tctttctctg 60
agaacagcga totggttatg gggcatttot gtototaa tgt cac tgt ctg ctg cat 116
                                           Cys His Cys Leu Leu His
tcc ctq caq aqc gac cgt gag aag tca gaa ggc ctt ccc gtg gcc ccg
                                                                   164
Ser Leu Gln Ser Asp Arg Glu Lys Ser Glu Gly Leu Pro Val Ala Pro
                                  15
             10
ttc atg gac cga gac aaa gtg acc aag gcc aca gcc cag att ggg ttc
                                                                   212
Phe Met Asp Arg Asp Lys Val Thr Lys Ala Thr Ala Gln Ile Gly Phe
                             3.0
```

| atc Ile | aag Lys 40 | ttt Phe | gtc Val | ctg Leu | atc Ile | cca Pro 45 | atg Met | ttt Phe | gaa Glu | aca Thr | gtg Val 50 | acc Thr | aag Lys | ctc Leu | ttc Phe | 260 |
|------------------|--------------------------------------|------------|------------------|------------------|------------------|------------------|------------|------------------|------------------|------------------|------------------|------------|-------------------|------------------|------------------|-----|
| ccc Pro 55 | atg Met | gtt Val | gag Glu | gag Glu | atc Ile 60 | atg Met | ctg Leu | cag Gln | cca Pro | ctt Leu 65 | tgg Trp | gaa Glu | tcc Ser | cga Arg | gat Asp 70 | 308 |
| cgc Arg | tac Tyr | gag Glu | gag Glu | ctg Leu 75 | aag Lys | cgg Arg | ata Ile | gat Asp | gac Asp 80 | gcc Ala | atg Met | aaa Lys | gag Glu | tta Leu 85 | cag Gln | 356 |
| aag Lys | aag Lys | act Thr | gac Asp 90 | agc Ser | ttg Leu | acg Thr | tct Ser | 999 Gly 95 | gcc Ala | acc Thr | gag Glu | aag Lys | tcc Ser 100 | aga Arg | gag Glu | 404 |
| | agc Ser | | | | | | | | | | | | tga | ggaaa | agc | 453 |
| ggg | gggc | gtg g | gctgo | cagtt | c to | ggac | gggct | . gg | ccgag | gctg | cgc | gggat | tcc t | tgt | gcaggg | 513 |
| aaga | agct | gcc (| ctggg | gcaco | ct gg | gcaco | cacaa | a gad | cat | gttt | tcta | aagaa | acc a | attti | tgttca | 573 |
| ctg | ataca | aaa a | aaaa | aaaa | aa aa | aaaa | a | | | , | | | | | | 599 |
| <21 <21 | 0 > 13 1 > 13 2 > PI 3 > Ho | 15 RT | sapie | ens | | | | | | | | | | | | |
| | 0> 1: His | | Leu | Leu 5 | His | Ser | Leu | Gln | Ser 10 | Asp | Arg | Glu | Lys | Ser 15 | Glu | |
| Gly | Leu | Pro | Val 20 | Ala | Pro | Phe | Met | Asp 25 | Arg | Asp | Lys | Val | Thr 30 | Lys | Ala | |
| Thr | Ala | Gln 35 | Ile | Gly | Phe | Ile | Lys 40 | Phe | Val | Leu | Ile | Pro 45 | Met | Phe | Glu | |
| Thr | Val 50 | Thr | Lys | Leu | Phe | Pro 55 | Met | Val | Glu | Glu | Ile 60 | Met | Leu | Gln | Pro | |
| Leu 65 | | ~ 7 | _ | 7 | 7.00 | Ara | Tvr | Glu | Glu | Leu | Lys | Arg | Ile | Asp | Asp | |
| • • • | Trp | Glu | Ser | arg | 70 | **** 5 | -1- | | | 75 | | | | | 80 | |
| | Trp Met | | | | 70 | | | | | 75 | Leu | Thr | Ser | Gly 95 | 80 | |
| Ala | | Lys | Glu | Leu 85 | 70 Gln | Lys | Lys | Thr | Asp 90 | 75 Ser | | | | 95 Glu | 80 Ala | |

```
<210> 14
<211> 28
<212> DNA
<213> Artificial Sequence
<223> Description of Artificial Sequence: primer
<400> 14
                                                                   28
aqtcgaattc accgtgagaa gtcagaag
<210> 15
<211> 28
<212> DNA
<213> Artificial Sequence
<223> Description of Artificial Sequence: primer
<400> 15
                                                                   28
gtcaaagctt acatggtctt gtggtgcc
<210> 16
<211> 1303
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> (107)..(1066)
<400> 16
aqtqactcta ctttgtgaaa atgtgaaact tcgtgtaggt actcagtaaa tcagtaaatt 60
                                                                   115
cttactaacq ttaqcccca gcctagctat ggagggtgca tgctga gcc ctg gag
                                                    Ala Leu Glu
cac atg tac cac gac ctc ggg ctg gtc agg gac ttc agc atc aac cct
                                                                   163
His Met Tyr His Asp Leu Gly Leu Val Arg Asp Phe Ser Ile Asn Pro
                         10
gtc acc ctc agg agg tgg ctg ttc tgc gtc cac gac aac tac aga aac
                                                                   211
Val Thr Leu Arg Arg Trp Leu Phe Cys Val His Asp Asn Tyr Arg Asn
                     25
                                                                    259
aac ccc ttc cac aac ttc cgg cac tgc ttc tgc gtg gcc cag atg atg
Asn Pro Phe His Asn Phe Arg His Cys Phe Cys Val Ala Gln Met Met
                 40
tac agc atg gtc tgg ctc tgc agt ctc cag gag aag ttc tca caa acg
                                                                   307
Tyr Ser Met Val Trp Leu Cys Ser Leu Gln Glu Lys Phe Ser Gln Thr
gat atc ctg atc cta atg aca gcg gcc atc tgc cac gat ctg gac cat
Asp Ile Leu Ile Leu Met Thr Ala Ala Ile Cys His Asp Leu Asp His
```

70 75 80

| ccc Pro | ggc Gly 85 | tac Tyr | aac Asn | aac Asn | acg Thr | tac Tyr 90 | cag Gln | atc Ile | aat Asn | gcc Ala | cgc Arg 95 | aca Thr | gag Glu | ctg Leu | gcg Ala | 403 |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|
| gtc Val 100 | cgc Arg | tac Tyr | aat Asn | gac Asp | atc Ile 105 | tca Ser | ccg Pro | ctg Leu | gag Glu | aac Asn 110 | cac His | cac His | tgc Cys | gcc Ala | gtg Val 115 | 451 |
| gcc Ala | ttc Phe | cag Gln | atc Ile | ctc Leu 120 | gcc Ala | gag Glu | cct Pro | gag Glu | tgc Cys 125 | aac Asn | atc Ile | ttc Phe | tcc Ser | aac Asn 130 | atc Ile | 499 |
| cca Pro | cct Pro | gat Asp | 999 Gly 135 | ttc Phe | aag Lys | cag Gln | atc Ile | cga Arg 140 | cag Gln | gga Gly | atg Met | atc Ile | aca Thr 145 | tta Leu | atc Ile | 547 |
| ttg Leu | gcc Ala | act Thr 150 | gac Asp | atg Met | gca Ala | aga Arg | cat His 155 | gca Ala | gaa Glu | att Ile | atg Met | gat Asp 160 | tct Ser | ttc Phe | aaa Lys | 595 |
| gag Glu | aaa Lys 165 | atg Met | gag Glu | aat Asn | ttt Phe | gac Asp 170 | tac Tyr | agc Ser | aac Asn | gag Glu | gag Glu 175 | cac His | atg Met | acc Thr | ctg Leu | 643 |
| ctg Leu 180 | aag Lys | atg Met | att Ile | ttg Leu | ata Ile 185 | aaa Lys | tgc Cys | tgt Cys | gat Asp | atc Ile 190 | tct Ser | aac Asn | gag Glu | gtc Val | cgt Arg 195 | 691 |
| cca Pro | atg Met | gaa Glu | gtc Val | gca Ala 200 | gag Glu | cct Pro | tgg Trp | gtg Val | gac Asp 205 | tgt Cys | tta Leu | tta Leu | gag Glu | gaa Glu 210 | tat Tyr | 739 |
| ttt Phe | atg Met | cag Gln | agc Ser 215 | gac Asp | cgt Arg | gag Glu | aag Lys | tca Ser 220 | gaa Glu | ggc Gly | ctt Leu | cct Pro | gtg Val 225 | gca Ala | ccg Pro | 787 |
| ttc Phe | arg Met | gac Asp 230 | cga Arg | gac Asp | aaa Lys | gtg Val | acc Thr 235 | aag Lys | gcc Ala | aca Thr | gcc Ala | cag Gln 240 | att Ile | gly aga | ttc Phe | 835 |
| atc Ile | aag Lys 245 | ttt Phe | gtc Val | ctg Leu | atc Ile | cca Pro 250 | atg Met | ttt Phe | gaa Glu | aca Thr | gtg Val 255 | acc Thr | aag Lys | ctc Leu | ttc Phe | 883 |
| ccc Pro 260 | Met | gtt Val | gag Glu | gag Glu | atc Ile 265 | atg Met | ctg Leu | cag Gln | cca Pro | ctt Leu 270 | tgg Trp | gaa Glu | tcc Ser | cga Arg | gat Asp 275 | 931 |
| cgc Arg | tac Tyr | gag Glu | gag Glu | ctg Leu 280 | aag Lys | cgg Arg | ata Ile | gat Asp | gac Asp 285 | Ala | atg Met | aaa Lys | gag Glu | tta Leu 290 | cag Gln | 979 |
| aag Lys | aag Lys | act Thr | gac Asp 295 | Ser | ttg Leu | acg Thr | tct Ser | 300 Gly 399 | Ala | acc Thr | gag Glu | aag Lys | tcc Ser 305 | aga Arg | gag Glu | 1027 |

aga agc aga gat gtg aaa aac agt gaa gga gac tgt gcc tgaggaaagc Arg Ser Arg Asp Val Lys Asn Ser Glu Gly Asp Cys Ala ggggggcgtg gctgcagttc tggacgggct ggccgagctg cgcgggatcc ttgtgcaggg 1136 aagagetgee etgggeacet ggeaceacaa gaceatgttt tetaagaace attttgttea 1196 ctgatacaaa aaaaaaaaag gaattcatga tgctgtacag aattttattt ttaaactgtc 1256 ttttaaataa tatattotta tacggaaaaa aaaaaaaaa aaaaaaa <210> 17 <211> 320 <212> PRT <213> Homo sapiens <400> 17 Ala Leu Glu His Met Tyr His Asp Leu Gly Leu Val Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe Cys Val His Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys Phe Cys Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu Gln Glu Lys Phe 50 Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu Glu Asn His His 105 Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu Cys Asn Ile Phe 120 115 Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg Gln Gly Met Ile 135 Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala Glu Ile Met Asp 155 145 150 Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser Asn Glu Glu His 170

1076

1303

Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val Asp Cys Leu Leu 200 195

Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile Ser Asn 185

| | ı Tyr | Phe | Met | Gln | Ser 215 | Asp | Arg | Glu | Lys | Ser 220 | Glu | Gly | Leu | Pro | |
|--|---|-------------------------------------|---|---|--|--|---|---------------------------------|--|--|--|--|--|---|-------------------|
| Val Al | a Pro | Phe | Met | Asp 230 | Arg | Asp | Lys | Val | Thr 235 | Lys | Ala | Thr | Ala | Gln 240 | |
| Ile Gl | / Phe | Ile | Lys 245 | Phe | Val | Leu | Ile | Pro 250 | Met | Phe | Glu | Thr | Val 255 | Thr | |
| Lys Le | ı Phe | Pro 260 | Met | Val | Glu | Glu | Ile 265 | Met | Leu | Gln | Pro | Leu 270 | Trp | Glu | |
| Ser Ar | g Asp 275 | Arg | Tyr | Glu | Glu | Leu 280 | Lys | Arg | Ile | Asp | Asp 285 | Ala | Met | Lys | |
| Glu Le 29 | | Lys | Lys | Thr | Asp 295 | Ser | Leu | Thr | Ser | Gly 300 | Ala | Thr | Glu | Lys | |
| Ser Ar 305 | g Glu | Arg | Ser | Arg 310 | Asp | Val | Lys | Asn | Ser 315 | Glu | Gly | Asp | Cys | Ala 320 | |
| <210><211><211><212><213> | 1887 DNA | sapie | ens | | | | | | | | | | | | |
| <220> <221> | CDS | | | | | | | | | | | | | | |
| <222> | (74). | . (167 | 72) | | | | | | | | | | | | |
| <400> | 18 | | | eg g | ctgg | cgtc | g gga | aaag | taca | gta | aaaa | gtc (| cgag | tgcagc | 60 |
| <400> | 18 cgcc | tcccç | gegge | gga ' | taa q | ggc' t | caa i | tcc . | agc | tac · | cgg (| ccc a | aag | gcc | 60 109 |
| <400> ctccc | 18 egee gege | tcccg agg a I | gcggo atg g Met (1 atc | gga Gly : | tcc (Ser (| ggc Gly ! | Ser : | tcc Ser | agc Ser ' | tac Tyr . gta | cgg Arg | pro 1 | aag Lys agc | gcc Ala aag | |
| ctcccc cgccgg atc ta Ile Ty tac tg | 18 cgcc gcgc c ctg r Leu 15 c aac | agg a agg a f gac Asp | gegge atg g Met (1 atc Ile | gga Gly gat Asp | gga Gly | ggc' f Gly f cgc Arg 20 | Ser | cag Gln | agc Ser ' aag Lys | tac Tyr gta Val | atc Ile 25 | ttc Phe | agc Ser | gcc Ala aag Lys ggc | 109 |
| ctcccc cgccgg atc ta Ile Ty tac tg | 18 cgcc cctgc cctgr Leu 15 caac s Asn 0 | agg a l gac Asp tcc Ser | gcggd atg G Met (1 atc Ile agc Ser | gga Gly gat Asp gac Asp | gga Gly atc Ile 35 | ggc fgly s | Ser | cag Gln ctg Leu | agc Ser aag Lys ttc Phe | tac Tyr gta Val tgc Cys 40 | atc Ile 25 atc Ile | ttc Phe gcc Ala | agc Ser acc Thr | gcc Ala aag Lys ggc Gly atg | 109 |
| ctg cc Leu Pr | 18 cgcc cctgc cctgr Leu 15 caac s Asn 0 t cgg o Arg | agg a l gac Asp tcc Ser aac Asn gac | atg General Action at Control | gga gat Asp gac Asp acc Thr | gga Gly atc Ile 35 atc Ile | ggc f Gly f cgc Arg 20 atg Met tcc Ser | Ser | cag Gln ctg Leu ctg | agc Ser aag Lys ttc Phe acc Thr 55 tca Ser | tac Tyr gta Val tgc Cys 40 acc Thr | atc Ile 25 atc Ile gac Asp | ttc Phe gcc Ala gac Asp | agc Ser acc Thr gcc Ala | aag Lys ggc Gly atg Met 60 | 109 157 205 |

| atc Ile | cag Gln | agc Ser 95 | gtg Val | ctg Leu | gcg Ala | cag Gln | gtt Val 100 | gca Ala | gag Glu | cag Gln | ttc Phe | tca Ser 105 | aga Arg | gca Ala | ttc Phe | 397 |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|
| aaa Lys | atc Ile 110 | aat Asn | gaa Glu | ctg Leu | aaa Lys | gct Ala 115 | gaa Glu | gtt Val | gca Ala | aat Asn | cac His 120 | ttg Leu | gct Ala | gtc Val | cta Leu | 445 |
| gag Glu 125 | aaa Lys | cgc Arg | gtg Val | gaa Glu | ttg Leu 130 | gaa Glu | gga Gly | cta Leu | aaa Lys | gtg Val 135 | gtg Val | gag Glu | att Ile | gag Glu | aaa Lys 140 | 493 |
| tgc Cys | aag Lys | agt Ser | gac Asp | att Ile 145 | aag Lys | aag Lys | atg Met | agg Arg | gag Glu 150 | gag Glu | ctg Leu | gcg Ala | gcc Ala | aga Arg 155 | agc Ser | 541 |
| agc Ser | agg Arg | acc Thr | aac Asn 160 | tgc Cys | ccc Pro | tgt Cys | aag Lys | tac Tyr 165 | agt Ser | ttt Phe | ttg Leu | gat Asp | aac Asn 170 | cac His | aag Lys | 589 |
| aag Lys | ttg Leu | act Thr 175 | cct Pro | cga Arg | cgc Arg | gat Asp | gtt Val 180 | ccc Pro | act Thr | tac Tyr | ccc Pro | aag Lys 185 | tac Tyr | ctg Leu | ctc Leu | 637 |
| tct Ser | cca Pro 190 | gag Glu | acc Thr | atc lle | gag Glu | gcc Ala 195 | ctg Leu | cgg Arg | aag Lys | ccg Pro | acc Thr 200 | ttt Phe | gac Asp | gtc Val | tgg Trp | 685 |
| ctt Leu 205 | tgg Trp | gag Glu | ccc Pro | aat Asn | gag Glu 210 | atg Met | ctg Leu | agc Ser | tgc Cys | ctg Leu 215 | gag Glu | cac His | atg Met | tac Tyr | cac His 220 | 733 |
| gac Asp | ctc Leu | gly aaa | ctg Leu | gtc Val 225 | agg Arg | gac Asp | ttc Phe | agc Ser | atc Ile 230 | ·aac Asn | cct Pro | gtc Val | acc Thr | ctc Leu 235 | agg Arg | 781 |
| agg Arg | tgg Trp | ctg Leu | ttc Phe 240 | tgc Cys | gtc Val | cac His | gac Asp | aac Asn 245 | tac Tyr | aga Arg | aac Asn | aac Asn | ccc Pro 250 | t.tc Phe | cac His | 829 |
| aac Asn | ttc Phe | cgg Arg 255 | cac His | tgc Cys | ttc Phe | tgc Cys | gtg Val 260 | gcc Ala | cag Gln | atg Met | atg Met | tac Tyr 265 | Ser | atg Met | gtc Val | 877 |
| tgg Trp | ctc Leu 270 | Cys | agt Ser | ctc Leu | cag Gln | gag Glu 275 | Lys | ttc Phe | tca Ser | caa Gln | acg Thr 280 | gat Asp | atc Ile | ctg Leu | atc Ile | 925 |
| cta Leu 285 | atg Met | aca Thr | gcg Ala | gcc Ala | atc Ile 290 | tgc Cys | cac His | gat Asp | ctg Leu | gac Asp 295 | His | ccc Pro | ggc | tac Tyr | aac Asn 300 | 973 |
| aac Asn | acg Thr | tac Tyr | cag Gln | atc Ile 305 | Asn | gcc Ala | cgc Arg | aca Thr | gag Glu 310 | Leu | gcg Ala | gtc Val | ago | tac Tyr 315 | Asn | 1021 |
| gac Asp | atc Ile | tca Ser | . ccg | ctg Leu | gag Glu | aac Asn | cac His | cac His | tgc Cys | gco Ala | gtg Val | gcc Ala | ttc Phe | cag Gln | atc Ile | 1069 |

320 325 330

| ctc Leu | gcc Ala | gag Glu 335 | cct Pro | gag Glu | tgc Cys | aac Asn | atc Ile 340 | ttc Phe | tcc Ser | aac Asn | atc Ile | cca Pro 345 | cct Pro | gat Asp | Gly aaa | 1117 |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|
| ttc Phe | aag Lys 350 | cag Gln | atc Ile | cga Arg | cag Gln | gga Gly 355 | atg Met | atc Ile | aca Thr | tta Leu | atc Ile 360 | ttg Leu | gcc Ala | act Thr | gac Asp | 1165 |
| atg Met 365 | gca Ala | aga Arg | cat His | gca Ala | gaa Glu 370 | att Ile | atg Met | gat Asp | tct Ser | ttc Phe 375 | aaa Lys | gag Glu | aaa Lys | atg Met | gag Glu 380 | 1213 |
| aat Asn | ttt Phe | gac Asp | tac Tyr | agc Ser 385 | aac Asn | gag Glu | gag Glu | cac His | atg Met 390 | acc Thr | ctg Leu | ctg Leu | aag Lys | atg Met 395 | att Ile | 1261 |
| ttg Leu | ata Ile | aaa Lys | tgc Cys 400 | tgt Cys | gat. Asp | atc Ile | tct Ser | aac Asn 405 | gag Glu | gtc Val | cgt Arg | cca Pro | atg Met 410 | gaa Glu | gtc Val | 1309 |
| gca Ala | gag Glu | cct Pro 415 | tgg Trp | gtg Val | gac Asp | tgt Cys | tta Leu 420 | tta Leu | gag Glu | gaa Glu | tat Tyr | ttt Phe 425 | atg Met | cag Gln | agc Ser | 1357 |
| gac Asp | cgt Arg 430 | gag Glu | aag Lys | tca Ser | gaa Glu | ggc Gly 435 | ctt Leu | cct Pro | gtg Val | Ala | ccg Pro 440 | ttc Phe | atg Met | gac Asp | cga Arg | 1405 |
| gac Asp 445 | aaa Lys | gtg Val | acc Thr | Lys | gcc Ala 450 | aca Thr | gcc Ala | cag Gln | att Ile | 999 Gly 455 | ttc Phe | atc Ile | aag Lys | ttt Phe | gtc Val 460 | 1453 |
| ctg Leu | atc Ile | cca Pro | atg Met | ttt Phe 465 | gaa Glu | aca Thr | gtg Val | acc Thr | aag Lys 470 | ctc Leu | ttc Phe | ccc Pro | atg Met | gtt Val 475 | gag Glu | 1501 |
| gag Glu | atc Ile | atg Met | ctg Leu 480 | Gln | cca Pro | ctt Leu | tgg Trp | gaa Glu 485 | tcc Ser | cga Arg | gat Asp | cgc Arg | tac Tyr 490 | gag Glu | gag Glu | 1549 |
| ctg Leu | aag Lys | cgg Arg 495 | ata Ile | gat Asp | gac Asp | gcc Ala | atg Met 500 | aaa Lys | gag Glu | tta Leu | cag Gln | aag Lys 505 | Lys | act Thr | gac Asp | 1597 |
| agc Ser | ttg Leu 510 | Thr | tct Ser | gly | gcc Ala | acc Thr 515 | Glu | aag Lys | tcc Ser | aga Arg | gag Glu 520 | Arg | agc Ser | aga Arg | gat Asp | 1645 |
| gtg Val 525 | Lys | aac Asn | agt Ser | gaa Glu | gga Gly 530 | Asp | tgt Cys | gcc Ala | tga | .ggaa | agc | ggg g | ggcg | tg | | 1692 |
| gct | gcag | ttc | tgga | .cggg | ct g | gccg | agct | g cg | cggg | atco | ttg | ıtgca | ıggg | aaga | ıgctgcc | 1752 |
| ctg | ggca | cct | ggca | ccac | aa g | acca | tgtt | t to | taag | aacc | att | ttgt | tca | ctga | taaaaa | 1812 |

aaaaaaaaa ggaattcatg atgctgtaca gaattttatt tttaaactgt cttttaaata 1872 atatattctt atacg

<210> 19

<211> 533

<212> PRT

<213> Homo sapiens

<400> 19

Met Gly Ser Gly Ser Ser Ser Tyr Arg Pro Lys Ala Ile Tyr Leu Asp 1 5 10 15

Ile Asp Gly Arg Ile Gln Lys Val Ile Phe Ser Lys Tyr Cys Asn Ser 20 25 30

Ser Asp Ile Met Asp Leu Phe Cys Ile Ala Thr Gly Leu Pro Arg Asn 35 40 45

Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val Ser Ile Asp 50 55 60

Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr Lys Val Arg Pro 65 70 75 80

Val Ala Ile Lys Gln Leu Ser Glu Arg Glu Glu Leu Ile Gln Ser Val 85 90 95

Leu Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu 100 105 110

Leu Lys Ala Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val 115 120 125

Glu Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp 130 135 140

Ile Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn 145 150 155 160

Cys Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro 165 170 175

Arg Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr

Ile Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro

Asn Glu Met Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu 210 215 220

Val Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe 225 230 235 240

Cys Val His Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His 245 250 255

Cys Phe Cys Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser 260 265 270

Leu Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala 275 280 285

Ala Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln 290 295 300

Ile Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro 305 310 315 320

Leu Glu Asn His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro

Glu Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile 340 345 350

Arg Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His 355 360 365

Ala Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr 370 375 380

Ser Asn Glu Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys 385 390 395 400

Cys Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp
405 410 415

Val Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys 420 425 . 430

Ser Glu Gly Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr 435 440 445

Lys Ala Thr Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met 450 455 460

Phe Glu Thr Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu 465 470 475 480

Gln Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile 485 490 495

Asp Asp Ala Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser 500 505 510

Gly Ala Thr Glu Lys Ser Arg Glu Arg Ser Arg Asp Val Lys Asn Ser 515 520 525

Glu Gly Asp Cys Ala 530

<210> 20

<211> 1967 <212> DNA

| <213 | > Ho | mo s | apie | ns | | | | | | | | | | | | |
|----------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|---------------------|-----|
| <220 <221 <222 | > CD | | 1741 |) | | | | | | | | | | | | |
| Ty | c ct | a aa | c at p Il | c ga e As | t gg p Gl 5 | ja cg y Ar | c at g Il | t ca e Gl | n Ly | g gt s Va 0 | a at 1 Il | c tt e Ph | c ag le Se | r Ly | g tac s Tyr 5 | 49 |
| tgc Cys | aac Asn | tcc Ser | agc Ser 20 | gac Asp | atc Ile | atg Met | gac Asp | ctg Leu 25 | ttc Phe | tgc Cys | atc Ile | gcc Ala | acc Thr 30 | ggc Gly | ctg Leu | 97 |
| cct Pro | cgg Arg | aac Asn 35 | acg Thr | acc Thr | atc Ile | tcc Ser | ctg Leu 40 | ctg Leu | acc Thr | acc Thr | gac Asp | gac Asp 45 | gcc Ala | atg Met | gtc Val | 145 |
| tcc Ser | atc Ile 50 | gac Asp | ccc Pro | acc Thr | atg Met | ccc Pro 55 | gcg Ala | aat Asn | tca Ser | gaa Glu | cgc Arg 60 | act Thr | ccg Pro | tac Tyr | aaa Lys | 193 |
| gtg Val 65 | aga Arg | cct Pro | gtg Val | gcc Ala | atc Ile 70 | aag Lys | caa Gln | ctc Leu | tcc Ser | gct Ala 75 | gat Asp | gtc Val | gag Glu | gac Asp | aag Lys 80 | 241 |
| aga Arg | acc Thr | aca Thr | agc Ser | cgt Arg 85 | ggc Gly | cag Gln | tct Ser | gct Ala | gag Glu 90 | aga Arg | cca Pro | ctg Leu | agg Arg | gac Asp 95 | aga Arg | 289 |
| cgg Arg | gtt Val | gtg Val | ggc Gly 100 | ctg Leu | gag Glu | cag Gln | ccc Pro | cgg Arg 105 | agg Arg | gaa Glu | gga Gly | gca Ala | ttt Phe 110 | gaa Glu | agt Ser | 337 |
| gga Gly | cag Gln | gta Val 115 | gag Glu | ccc Pro | agg Arg | ccc Pro | aga Arg 120 | gag Glu | ccc Pro | cag Gln | ggc Gly | tgc Cys 125 | tac Tyr | cag Gln | gaa Glu | 385 |
| ggc Gly | cag Gln 130 | cgc Arg | atc Ile | cct Pro | cca Pro | gag Glu 135 | aga Arg | gaa Glu | gaa Glu | tta Leu | atc Ile 140 | cag Gln | agc Ser | gtg Val | ctg Leu | 433 |
| gcg Ala 145 | cag Gln | gtt Val | gca Ala | gag Glu | cag Gln 150 | ttc Phe | tca Ser | aga Arg | gca Ala | ttc Phe 155 | aaa Lys | atc Ile | aat Asn | gaa Glu | ctg Leu 160 | 481 |
| aaa Lys | gct Ala | gaa Glu | gtt Val | gca Ala 165 | aat Asn | cac His | ttg Leu | gct Ala | gtc Val 170 | cta Leu | gag Glu | aaa Lys | cgc Arg | gtg Val 175 | gaa Glu | 529 |
| ttg Leu | gaa Glu | gga Gly | cta Leu 180 | aaa Lys | gtg Val | gtg Val | gag Glu | att Ile 185 | gag Glu | aaa Lys | tgc Cys | aag Lys | agt Ser 190 | gac Asp | att Ile | 577 |
| aag Lys | aag Lys | atg Met 195 | agg Arg | gag Glu | gag Glu | ctg Leu | gcg Ala 200 | gcc Ala | aga Arg | agc Ser | agc Ser | agg Arg 205 | acc Thr | aac Asn | tgc Cys | 625 |
| | | | | | | | | | | | | | | | | |

| | ccc Pro | tgt Cys 210 | aag Lys | tac Tyr | agt Ser | ttt Phe | ttg Leu 215 | gat Asp | aac Asn | cac His | aag Lys | aag Lys 220 | ttg Leu | act Thr | cct Pro | cga Arg | 673 |
|---|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|
| | cgc Arg 225 | gat Asp | gtt Val | ccc Pro | act Thr | tac Tyr 230 | ccc Pro | aag Lys | tac Tyr | ctg Leu | ctc Leu 235 | tct Ser | cca Pro | gag Glu | acc Thr | atc Ile 240 | 721 |
| | gag Glu | gcc Ala | ctg Leu | cgg Arg | aag Lys 245 | ccg Pro | acc Thr | ttt Phe | ga,c Asp | gtc Val 250 | tgg Trp | ctt Leu | tgg Trp | gag Glu | ccc Pro 255 | aat Asn | 769 |
| | gag Glu | atg Met | ctg Leu | agc Ser 260 | tgc Cys | ctg Leu | gag Glu | cac His | atg Met 265 | tac Tyr | cac Hıs | gac Asp | ctc Leu | 999 Gly 270 | ctg Leu | gtc Val | 817 |
| | agg Arg | gac Asp | ttc Phe 275 | agc Ser | atc Ile | aac Asn | cct Pro | gtc Val 280 | acc Thr | ctc Leu | agg Arg | agg Arg | tgg Trp 285 | ctg Leu | ttc Phe | tgc Cys | 865 |
| | gtc Val | cac His 290 | gac Asp | aac Asn | tac Tyr | aga Arg | aac Asn 295 | aac Asn | ccc Pro | ttc Phe | cac His | aac Asn 300 | ttc Phe | cgg Arg | cac His | tgc Cys | 913 |
| • | ttc Phe 305 | tgc Cys | gtg Val | gcc Ala | cag Gln | atg Met 310 | atg Met | tac Tyr | agc Ser | atg Met | gtc Val 315 | tgg Trp | ctc Leu | tgc Cys | agt Ser | ctc Leu 320 | 961 |
| | cag Gln | gag Glu | aag Lys | ttc Phe | tca Ser 325 | caa Gln | acg Thr | gat Asp | atc Ile | ctg Leu 330 | atc Ile | cta Leu | atg Met | aca Thr | gcg Ala 335 | gcc Ala | 1009 |
| - | atc Ile | tgc Cys | cac His | gat Asp 340 | ctg Leu | gac Asp | cat His | ccc Pro | ggc Gly 345 | tac Tyr | aac Asn | aac Asn | acg Thr | tac Tyr 350 | cag Gln | atc Ile | 1057 |
| | aat Asn | gcc Ala | cgc Arg 355 | aca Thr | gag Glu | ctg Leu | gcg Ala | gtc Val 360 | cgc Arg | tac Tyr | aat Asn | gac Asp | atc Ile 365 | tca Ser | ucg Pro | ctg Leu | 1105 |
| | gag Glu | aac Asn 370 | cac His | cac His | tgc Cys | gcc Ala | gtg Val 375 | gcc Ala | ttc Phe | cag Gln | atc Ile | ctc Leu 380 | gcc Ala | gag Glu | cct Pro | gag Glu | 1153 |
| | tgc Cys 385 | aac Asn | atc Ile | ttc Phe | tcc Ser | aac Asn 390 | atc Ile | cca Pro | cct Pro | gat Asp | ggg Gly 395 | ttc Phe | aag Lys | cag Gln | atc Ile | cga Arg 400 | 1201 |
| | cag Gln | gga Gly | atg Met | atc Ile | aca Thr 405 | tta Leu | atc Ile | ttg Leu | gcc Ala | act Thr 410 | Asp | atg Met | gca Ala | aga Arg | cat His 415 | gca Ala | 1249 |
| | gaa Glu | att Ile | atg Met | gat Asp 420 | tct Ser | ttc Phe | aaa Lys | gag Glu | aaa Lys 425 | Met | gag Glu | aat Asn | ttt Phe | gac Asp 430 | Tyr | agc Ser | 1297 |
| | aac Asn | gag Glu | gag Glu | cac His | atg Met | acc Thr | ctg Leu | ctg Leu | aag Lys | atg Met | att Ile | ttg Leu | ata Ile | aaa Lys | tgc Cys | tgt Cys | 1345 |

| 435 440 | • | 445 |
|---------|---|-----|
|---------|---|-----|

| gat Asp | atc Ile 450 | tct Ser | aac Asn | gag Glu | gtc Val | cgt Arg 455 | cca Pro | atg Met | gaa Glu | gtc Val | gca Ala 460 | gag Glu | cct Pro | tgg Trp | gtg Val | 1393 |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|
| gac Asp 465 | tgt Cys | tta Leu | tta Leu | gag Glu | gaa Glu 470 | tat Tyr | ttt Phe | atg Met | cag Gln | agc Ser 475 | gac Asp | cgt Arg | gag Glu | aag Lys | tca Ser 480 | 1441 |
| gaa Glu | ggc Gly | ctt Leu | cct Pro | gtg Val 485 | gca Ala | ccg Pro | ttc Phe | atg Met | gac Asp 490 | cga Arg | gac Asp | aaa Lys | gtg Val | acc Thr 495 | aag Lys | 1489 |
| gcc Ala | aca Thr | gcc Ala | cag Gln 500 | att Ile | Gly 999 | ttc Phe | atc Ile | aag Lys 505 | ttc Phe | gtc Val | ctg Leu | atc Ile | cca Pro 510 | atg Met | ttt Phe | 1537 |
| gaa Glu | aca Thr | gtg Val 515 | acc Thr | aag Lys | ctc Leu | ttc Phe | ccc Pro 520 | atg Met | gtt Val | gag Glu | gag Glu | atc Ile 525 | atg Met | ctg Leu | cag Gln | 1585 |
| cca Pro | ctt Leu 530 | tgg Trp | gaa Glu | tcc Ser | cga Arg | gat Asp 535 | cgc Arg | tac Tyr | gag Glu | gag Glu | ctg Leu 540 | aag Lys | cgg Arg | ata Ile | gat Asp | 1633 |
| gac Asp 545 | gcc Ala | atg Met | aaa Lys | gag Glu | tta Leu 550 | cag Gln | aag Lys | aag Lys | act Thr | gac Asp 555 | agc Ser | ttg Leu | acg Thr | tct Ser | 999 Gly 560 | 1681 |
| gcc Ala | acc Thr | gag Glu | aag Lys | tcc Ser 565 | aga Arg | gag Glu | aga Arg | agc Ser | aga Arg 570 | gat Asp | gtg Val | aaa Lys | aac Asn | agt Ser 575 | gaa Glu | 1729 |
| | gac Asp | | | | ggaa | agc (| 3 333 | ggcg | tg g | ctgc | agtt | c tg | gacg | ggct | | 1781 |
| ggc | cgag | ctg | cgcg | ggat | cc t | tgtg | cagg | g aa | gagc | tgcc | ctg | ggca | cct | ggca | ccacaa | 1841 |
| gac | catg | ttt | tcta | agaa | cc a | tttt | gttc | a ct | gata | caaa | aaa | aaaa | aaa | ggaa | ttcatg | 1901 |
| atg | ctgt | aca | gaat | ttta | tt t | ttaa | actg | t ct | ttta | aata | ata | tatt | ctt | atac | ggaaaa | 1961 |
| aaa | aaa | | | | | | | | | | | | | | | 1967 |

<210> 21 <211> 580

<212> PRT

<213> Homo sapiens

<400> 21

Tyr Leu Asp Ile Asp Gly Arg Ile Gln Lys Val Ile Phe Ser Lys Tyr 1 5 10 15

Cys Asn Ser Ser Asp Ile Met Asp Leu Phe Cys Ile Ala Thr Gly Leu 25 20

- Pro Arg Asn Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val 35

 Ser Ile Asp Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr Lys
- Val Arg Pro Val Ala Ile Lys Gln Leu Ser Ala Asp Val Glu Asp Lys
 65 70 75 80
- Arg Thr Thr Ser Arg Gly Gln Ser Ala Glu Arg Pro Leu Arg Asp Arg 90 95
- Arg Val Val Gly Leu Glu Gln Pro Arg Arg Glu Gly Ala Phe Glu Ser
- Gly Gln Val Glu Pro Arg Pro Arg Glu Pro Gln Gly Cys Tyr Gln Glu 115 120 125
- Gly Gln Arg Ile Pro Pro Glu Arg Glu Glu Leu Ile Gln Ser Val Leu 130 135 140
- Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu Leu 145 150 155 160
- Lys Ala Glu Val Ala Asn His Leu Ala Val Leu Clu Lys Arg Val Glu 165 170 175
- Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp Iie 180 185 190
- Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn Cys
 195 200 205
- Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro Arg 210 215 220
- Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr Ile 225 230 235 240
- Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro Asn 245 250 255
- Glu Met Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu Val 260 265 270
- Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe Cys 275 280 285
- Val His Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys 290 295 300
- Phe Cys Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu 305 310 315 320
- Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala 325 330 335
- Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile

340 345 350

Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu 355 360 365

Glu Asn His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu 370 375 380

Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg 385 390 395 400

Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala 405 410 415

Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser 420 425 430

Asn Glu Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys 435 440 . 445

Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val 450 455 460

Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys Ser 465 470 475 480

Glu Gly Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys
485 490 495

Ala Thr Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe 500 505 510

Glu Thr Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln 515 520 525

Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp 530 540

Asp Ala Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly 545 550 560

Ala Thr Glu Lys Ser Arg Glu Arg Ser Arg Asp Val Lys Asn Ser Glu 565 570 575

Gly Asp Cys Ala 580

<210> 22

<211> 1457

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (164)..(1453)

<400> 22

ggctcccggg cgtcccgggc ccggtggcgg cgcggctgtg gttggctgag cgccgcgggc 60 cgcccccgc ccgcccctc cctgctccc ctccccgcc tcccgcggcg gctggcgtcg 120 175 qqaaaqtaca gtaaaaagtc cgagtgcagc cgccgggcgc agg atg gga tcc ggc Met Gly Ser Gly tcc tcc agc tac cgg ccc aag gcc atc tac ctg gac atc gat gga cgc 223 Ser Ser Ser Tyr Arg Pro Lys Ala Ile Tyr Leu Asp Ile Asp Gly Arg att cag aag gta atc ttc agc aag tac tgc aac tcc agc gac atc atg 271 Ile Gln Lys Val Ile Phe Ser Lys Tyr Cys Asn Ser Ser Asp Ile Met gac ctg ttc tgc atc gcc acc ggc ctg cct cgg aac acg acc atc tcc 319 Asp Leu Phe Cys Ile Ala Thr Gly Leu Pro Arg Asn Thr Thr Ile Ser ctg ctg acc acc gac gac gcc atg gtc tcc atc gac ccc acc atg ccc 367 Leu Leu Thr Thr Asp Asp Ala Met Val Ser Ile Asp Pro Thr Met Pro gcg aat tca gaa cgc act ccg tac aaa gtg aga cct gtg gcc atc aag 415 Ala Asn Ser Glu Arg Thr Pro Tyr Lys Val Arg Pro Val Ala Ile Lys caa ctc tcc gag aga gaa gaa tta atc cag agc gtg ctg gcg cag gtt 463 Gln Leu Ser Glu Arg Glu Glu Leu Ile Gln Ser Val Leu Ala Gln Val 95 gca gag cag ttc tca aga gca ttc aaa atc aat gaa ctg aaa gct gaa 511 Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu Leu Lys Ala Glu gtt gca aat cac ttg gct gtc cta gag aaa cgc gtg gaa ttg gaa gga 559 Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val Glu Leu Glu Gly 125 cta aaa gtg gtg gag att gag aaa tgc aag agt gac att aag aag atg 607 Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp Ile Lys Lys Met agg gag gag ctg gcg gcc aga agc agc agg acc aac tgc ccc tgt aag 655 Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn Cys Pro Cys Lys 155 703 tac agt ttt ttg gat aac cac aag aag ttg act cct cga cgc gat gtt Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro Arg Arg Asp Val 170 751 ccc act tac ccc aag tac ctg ctc tct cca gag acc atc gag gcc ctg Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr Ile Glu Ala Leu 190 cgg aag ccg acc ttt gac gtc tgg ctt tgg gag ccc aat gag atg ctg 799 Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro Asn Glu Met Leu

200 205 210

| agc Ser | tgc Cys | ctg Leu 215 | gag Glu | cac His | atg Met | tac Tyr | cac His 220 | gac Asp | ctc Leu | ggg Gly | ctg Leu | gtc Val 225 | agg Arg | gac Asp | ttc Phe | 847 |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|
| agc Ser | atc Ile 230 | aac Asn | cct Pro | gtc Val | acc Thr | ctc Leu 235 | agg Arg | agg Arg | tgg Trp | ctg Leu | ttc Phe 240 | tgc Cys | gtc Val | cac His | gac Asp | 895 |
| aac Asn 245 | tac Tyr | aga Arg | aac Asn | aac Asn | ccc Pro 250 | ttc Phe | cac His | aac Asn | ttc Phe | cgg Arg 255 | cac His | tgc Cys | ttc Phe | tgc Cys | gtg Val 260 | 943 |
| gcc Ala | cag Gln | atg Met | atg Met | tac Tyr 265 | agc Ser | atg Met | gtc Val | tgg Trp | ctc Leu 270 | tgc Cys | agt Ser | ctc Leu | cag Gln | gag Glu 275 | aag Lys | 991 |
| ttc Phe | tca Ser | caa Gln | acg Thr 280 | gat Asp | atc Ile | ctg Leu | atc Tle | cta Leu 285 | atg Met | aca Thr | gcg Ala | gcc Ala | atc Ile 290 | tgc Cys | cac His | 1039 |
| gat Asp | ctg Leu | gac Asp 295 | cat His | ccc Pro | ggc Gly | tac Tyr | aac Asn 300 | aac Asn | acg Thr | tac Tyr | cag Gln | atc Ile 305 | aat Asn | gcc Ala | cgc Arg | 1087 |
| aca Thr | gag Glu 310 | ctg Leu | gcg Ala | gtc Val | cgc Arg | tac Tyr 315 | aat Asn | gac Asp | atc Ile | tca Ser | ccg Pro 320 | ctg Leu | gag Glu | aac Asn | cac His | 1135 |
| cac His 325 | tgc Cys | gcc Ala | gtg Val | gcc Ala | ttc Phe 330 | cag Gln | atc Ile | ctc Leu | gcc Ala | gag Glu 335 | cct Pro | gag Glu | tgc Cys | aac Asn | atc Ile 340 | 1183 |
| ttc Phe | tcc Ser | aac Asn | atc Ile | cca Pro 345 | cct Pro | gat Asp | gly aaa | ttc Phe | aag Lys 350 | cag Gln | atc Ile | cga Arg | cag Gln | gga Gly 355 | atg Met | 1231 |
| atc Ile | aca Thr | tta Leu | atc Ile 360 | ttg Leu | gcc Ala | act Thr | gac Asp | atg Met 365 | gca Ala | aga Arg | cat His | gca Ala | gaa Glu 370 | Ile | atg Met | 1279 |
| gat Asp | tct Ser | ttc Phe 375 | aaa Lys | gag Glu | aaa Lys | atg Met | gag Glu 380 | Asn | ttt Phe | gac Asp | tac Tyr | agc Ser 385 | Asn | gag Glu | gag Glu | 1327 |
| cac His | atg Met 390 | Thr | ctg Leu | ctg | aag Lys | atg Met 395 | Ile | ttg Leu | ata Ile | aaa Lys | tgc Cys 400 | Cys | gat Asp | atc Ile | tct Ser | 1375 |
| aac Asn 405 | Glu | gtc Val | cgt Arg | cca Pro | atg Met 410 | Glu | gto Val | gca Ala | gag Glu | cct Pro 415 | Trp | gtg Val | gac Asp | tgt Cys | tta Leu 420 | 1423 |
| tta Leu | gag Glu | gaa Glu | tat Tyr | ttt Phe 425 | Met | cag Gln | ago Ser | gac Asp | cgt Arg 430 | i | ја | | | | | 1457 |

<210> 23 <211> 430

<212> PRT

<213> Homo sapiens

<400> 23

Met Gly Ser Gly Ser Ser Ser Tyr Arg Pro Lys Ala Ile Tyr Leu Asp 1 5 10 15

Ile Asp Gly Arg Ile Gln Lys Val Ile Phe Ser Lys Tyr Cys Asn Ser 20 25 30

Ser Asp Ile Met Asp Leu Phe Cys Ile Ala Thr Gly Leu Pro Arg Asn 45

Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val Ser Ile Asp 50 55 60

Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr Lys Val Arg Pro .65 70 75 80

Val Ala Ile Lys Gln Leu Ser Glu Arg Glu Glu Leu Ile Gln Ser Val 85 90 95

Leu Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu 100 105 110

Leu Lys Ala Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val 115 120 125

Glu Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp 130 135 140

Ile Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn 145 . 150 . 155 . 160

Cys Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro 165 170 175

Arg Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr
180 185 190

Ile Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro 195 200 205

Asn Glu Met Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu 210 215 220

Val Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe 225 230 235 240

Cys Val His Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His 245 250 255

Cys Phe Cys Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser 260 265 270

Leu Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala

275 280 285

Ala Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln 290 295 300

Ile Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro 305 310 315 320

Leu Glu Asn His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro 325 330 335

Glu Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile 340 345 350

Arg Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His 355 360 365

Ala Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr 370 375 380

Ser Asn Glu Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys 385 390 395 400

Cys Aso Ile Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp 405 410 415

Val Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg 420 425 430

<210> 24

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: FLAG epitope

<400> 24

Asp Thr Lys Asp Asp Asp Lys

<210> 25

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 25

tagaccatgg actacaagga cgacgatgac aagatggacg cattcagaag cact

54

<210> 26

<211> 18

<212> DNA

```
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 26
cgaggagtca acttcttg
```

18